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GTTCACGC

1
10 AGCAGTACCACACCACGATCAACCGCATATTTCAGTTTGGAGCACATTGCCAATTTCAAGATGTTGACAAAGTTGGCTCTATGGCACTACCACCTCTACTGGGAGGATGTGT
125 ACCCTGTATTGATCGTGGAGGATGTGAGCTCCACAACTGCACGCTGGAGTTTCGGTTACCGTATCGCAATTCGAATTACAACTCCAACTACAGCGACTTGTGTGCTGATGCG
240 TGAAGCAACGGCTTTCGGCTGCTGAACGGTACAGAGAGTTTTCGATATGGAACGGAGAGACTTTTCAAGTTTGGAGAGCTTACGGTCACTGTGGCGAGAGGGAGTCTC
355 AACAGCAGCGTATGTCAACGGTTCAAGACTGGCACTTCCGAGACTAAGAGCATTTGGGGTTCTTGCAGGAGGGCGCATACACCTATGCCATTGGTTTGGAAAGTTGC
470 CGACAAACAGCTACGTTGCGGTTACTAGACATGCGAGTGGATTACGAGCTCGTACCGGGAGAGAGCATTTGAAGGAGGCCAATAGATACTTTCCATTCTCTGATGTGAAGATAC
585 ATAGACCATAAAGCACAAGGCTCGGAATATATACGGTATAGACTCTACTAATAACATCCAAACAGAGTGAATAAATAAATAACACACAAACAGAAATAAACAACGA
700 ACCACTTACAGAGCCATCTCTACACACACCAATGTACTGGGTGCTACTCTCTTTCGTGTCGATATGTCATGCGCAACACCGGAGACATGCTTGGTACGGGTGCCGAGTACTAC
815 AATATTGTACCGACCCCTCACCCATATCCAGGATGCCAGGTTCACTGGGAGCTCCATCGTCTCAACACCCACACACAGTACTACTAGACTACCCCATTTGGATCTATCGAGG
930 ACCAGGATATGTCACACATAATCACAGTCACATACGATACCGTTGGCAACACCGATCAACACTACTAGTCGGGTGAACACTACGGAGACATACGTTTACGACGGCGACAT
1045 GCTCACATTAAGCTATGCTGGCGCCACCATGCCGTAGCACTTTAGCATTGACATGCTGTATATGCACAGCAACGGATTGCTTCCCAATTGTAGTGAACAAATGCCAGTAGATTCTTAC
1160 GTGGCGGTACCTACGAGTTCCATGCCCTTAGTTATGACAAATGGCAGGTTTTCGAAGAGAAACGGCATTTGCTTCCCATATTGGTTAAGGCTGTATTAGAGCCGTGGGGCAGTA
1275 CCATTCCATTGGAGTTGTACGAACAATCGTGTATTAGTAGATATCACATATTTCATTGCTGGAACATCTTCCCATATTGGTTAAGGCTGTATTAGAGCCGTGGGGCAGTA
1390 GTGTGCGTTATATTTAGCAAAATAAACAATGATTTTATCAAGTCGATAGCCTTATACATTTAGCTGATATGTTTGTCTATAGGTTTAAATGATATTGTTAGATTTA
1505 AGGTTTGTGTAGCTGGCAAGTTTATAGATGCCAATTCGTTGGGTGCTGTTCACTACCAATACTGCAGTAATAAGAGTTTGAATCTTTGTATATATTTAGCTCATTCCGAG
1620 ATCAATAATTCGTTCTTTCTTAGTGCCACACTACCAAAAGGTTATGGTTAAGAGGACACCGTGCATTTCCTGTTCCCTAAGCCAATGACATACCGCTCTCCCAATATA
1735 AGAGATCGGGGCTTGAAACGTTTTCAGATGAAGTTATGCGAAGTCTTGTGCTCTATGATGCGAGCAAGATTAGTTGCACCAATATATACAGGACAGAAAGTTCAAAAGTTGGAAA

FIG. 1A

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1850 ATTATATGAATGTATCCTGATAGCGGAACTATGGGCGCTAAATGTCAATCACCAGCAAAAGATATACCTAAGTTAAGAGAAACATCAATGATAAAGTGTCTCTCCCCATG
1965 GGTGATATAGTAGGACCTTACTTCATGAATTAACACACAATTTGTATATAGTCTCAGCATAGTCTTACAAAGTTTGGACAAACTAAAGTCGAGATACGACGACATACAT
2080 GTAGGGAGCCAAACAAATATTTATCCGAGCAAAACAGGTTGGTAGAGTGTATATATCCGGAAGTTAGTATCTGTACAGAGACAAAGGCTCAAGGAATTAAGCAAAACC
2195 AAAGTTTGGCAATGAAGCAAAAGTTTNGAGCTGAATTCAAAAATTAATAACCTATCGGTGGCTGCCAAGGATCTTAGACAGCAATTTCTAGAGCGGCAGAGCGTGGTTG
2310 AGACATTCAAAATGGTGTATAGTGAATTCAGAAATGCCAGAAACCGAANGTCTCCAAAGAGGACGAGTAGCACACAATCAGGTGGAGCTTATCGGTCTACAGAGGTAACACAGTTG
2425 GAACATTTCCTAATGATTCATTGATTTTACATCGGACACTGAGAACTCCAAATTCACCTGATTAACCGGAACCGCCGATACCTCCAGGAGATAATTTGATTTAACTTCAGATAC
2540 AGAAGACATAGAGCCACATCACCAGAGGTAATGATATAGATTAAGTTAAATATAAGGCAATATATTGCCAATGTATACTCTTTAACAGTGTGTCTCTGCAAGGATT
2655 AAGCACCAGAAAAAATATGTGGATCGGTGTTATAGTTTACTCTTTCTGAAAAGAAACATTAAAGTGTCTTACTAGTTGTCACTACGACACAGTCCCTGAA
29 Met Ser Phe Ala Arg Tyr Ile Tyr Tyr Thr Ile Ala Val Ala Val Leu Leu Asn Phe Val Lys Ala Thr Glu Asn Asn Phe Lys
2770 ATG TCA TTT GCA AGG TAT ATC TAC TAC ACC ATT GCG GTT GCT GTT TTA TTA AAT TTT GTC AAA GCT ACT GAA AAT AAC AAT TTT AAA
Leu Glu Val Glu Ala Ser Trp Ser Asn Ile Asp Phe Leu Pro Ser Phe Ile Glu Ala Ile Val Gly Phe Asn Asp Ser Leu Tyr Glu
2857 CTT GAA GTT GAA GCG TCA TGG AGC AAT ATT GAT TTC CTT CCT AGC TTT ATA GAG GCC ATC GTT GGC TTC AAT GAC TCT TTG TAC GAA
Gln Thr Ile Glu Thr Ile Phe Gly Leu Gly Asp Thr Glu Val Glu Leu Glu Asp Ala Ser Asp Gln Glu Ile Tyr Ser Thr Val
2944 CAG ACA ATT GAA ACA ATT TTT GGT TTA GGA GAC ACT GAA GTG GAA TTA GAA GAT GAT GCT TCA GAT CAA GAA ATA TAT TCT ACC GTG
Ile Asn Ser Leu Gly Leu Thr Asp Gln Asp Leu Asp Phe Ile Asn Phe Asp Leu Thr Asn Lys His Thr Pro Arg Ile Ala Ala
3031 ATC AAC TCA TTA GGG' TTA ACA GAT CAA GAT TTG GAT TTT AAT TTT GAT TTA ACC AAC AAA AAA CAT ACA CCA AGA ATC GCA GCC
His Tyr Asp His Tyr Ser Asp Val Leu Thr Lys Phe Gly Asp Arg Leu Lys Ser Glu Cys Ala Lys Asp Ser Phe Gly Asn Ala Val
3118 CAT TAC GAT CAC TAT TCT GAT GTT CTA ACT AAG TTT GGC GAT CGA CTC AAA AGT GAA TGT GCA AAA GAC TCT TTT GGG AAT GCA GTG
Glu Thr Lys Asn Gly Gln Ile Gln Thr Trp Leu Tyr Asn Asp Lys Ile Tyr Cys Ser Ala Asn Asp Leu Phe Ala Leu Arg Thr

~~FE~~ - 1A (cont.)

3205 GAA ACG AAA AAT GGT CAA ATT CAA ACG TGG TTA CTA TAT AAC GAT AAG ATA TAT TGT TCG GCT AAT GAT TTG TTT GCA TTA CGA ACT
 Asp Leu Ser Ser His Ser Thr Leu Leu Phe Asp Arg Ile Ile Gly Lys Ser Lys Asp Ala Pro Leu Val Ile Leu Tyr Gly Ser Pro 203
 3292 GAT TTG AGT TCT CAT TCT ACA CTT TTA TTT GAT AGG ATT ATT GGA AAA TCA AAA GAT GCA CCT TTG GTG ATT TTA TAT GGA AGC CCG
 Thr Glu Glu Leu Thr Lys Asp Phe Leu Lys Ile Leu Tyr Pro Asp Ala Lys Ala Gly Lys Leu Lys Phe Val Trp Arg Tyr Ile Pro 232
 3379 ACT GAG GAA CTG ACT AAA GAT TTT CTT AAA ATA TTG TAT CCA GAT GCA AAG GCT GGA AAA TTA ANG TTT GTA TCG AGG TAC ATT CCA
 Leu Gly Ile Lys Lys Leu Asp Ser Ile Ser Gly Tyr Gly Val Ser Leu Lys Met Glu Lys Tyr Asp Tyr Ser Gly Ala Glu Gly Asn 261
 3466 CTG GGA ATC AAA AAA CTG GAC TCA ATT TCT GCA TAC TCA TTA TTA AAA ATG GAA AAG TAT GAT TAT TCT GGT GCA GAA GGA AAT
 Pro Lys Tyr Asp Leu Ser Arg Asp Phe Thr Arg Ile Asn Asp Ser Gln Glu Leu Val Asn Glu Lys His Ser Tyr Glu Leu 290
 3553 CCA AAG TAT GAT TTG AGT CGA GAT TTC ACC ACA ATT AAT GAC TCG CAA GAG TTG GTC CTG GTC AAT GAA AAA CAT TCG TAT GAA CTT
 Gly Val Lys Leu Thr Ser Phe Ile Leu Ser Asn Arg Tyr Lys Ser Thr Lys Tyr Asp Leu Leu Asp Thr Ile Leu Thr Asn Phe Pro 319
 3640 GGT GTT AAA TTG ACT TCA TTC ATA TTA TCC AAT CGT TAC AAG ACT AAA TAT GAC CTT TTA GAT ACG ATT TTA ACC AAC TTT CCC
 Lys Phe Ile Pro Tyr Ile Ala Arg Leu Pro Lys Leu Leu Asn His Glu Lys Val Lys Ser Lys Val Leu Gly Asn Glu Asp Ile Gly 348
 3727 AAG TTT ATT CCT TAC ATT GCA CGA TTA CCA AAA TTA CTA AAT CAT GAA AAA GTT AAA TCC AAA GTG CTT GCA AAT GAA GAT ATA GGG
 Leu Ser Gln Asp Ser Tyr Gly Ile Tyr Ile Asn Gly Ser Pro Ile Asn Pro Leu Glu Leu Asp Ile Tyr Asn Leu Gly Thr Arg Ile 377
 3814 CTA TCT CAA GAC TCC TAC GCA ATA TAT ATC AAC GGT TCC CCA ATA AAT CCA CTA GAG TTA GAT ATT TAC AAT CTA GGT ACC AGG ATA
 Lys Glu Glu Leu Gln Thr Val Lys Asp Leu Val Lys Leu Gly Phe Asp Thr Val Gln Ala Lys Leu Ile Ala Lys Phe Ala Leu 406
 3901 ANG GAG GAA TTA CAG ACT GTG AAA GAT TTA GTG NAA CTT GGA TTT GAT ACC GTA CAA GCA AAG CTC TTG ATA GCA AAA TTT GCT TTA
 Leu Ser Ala Val Lys Gln Thr Phe Arg Asn Gly Asn Thr Leu Met Gly Asn Asn Glu Asn Arg Phe Lys Val Tyr Glu Asn Glu 435
 3988 CTT TCA GCT GTT AAA CAA ACA CAA TTT CGA AAT GGG AAT ACA TTA ATG GGT AAC AAT GAA AAT AGA TTT AAA GTG TAT GAA AAT GAA
7100 - 1A (cont.)

WO 00/68420

PCT/CA00/00533

464 Phe Lys Lys Gly Ser Ser Glu Lys Gly Gly Val Leu Phe Phe Asn Asn Ile Glu Leu Asp Asn Thr Phe Lys Glu Tyr Thr Thr Asp
4075 TTT AAG AAG GGT AGT TCA GAA AAG GGT GGG GTC TTG TTT TTC AAT AAC ATT GAA TTA GAC AAC ACA TTC AAG GAG TAC ACC ACT GAT
Arg Glu Glu Ala Tyr Leu Gly Val Gly Ser His Lys Lys Leu Lys Pro Asn Gln Ile Pro Leu Leu Lys Glu Asn Ile His Asp Leu Ile
4162 CGT GAG GAG GCA TAT TTA GCA GTT GGT TCT CAT AAA CTT AAG CCA AAT CAA ATT CCG TTA TTG AAA GAG AAC ATC CAT GAT TTA ATT
522 Phe Ala Leu Asn Phe Gly Asn Lys Asn Gln Leu Arg Val Phe Thr Leu Ser Lys Val Ile Leu Asp Ser Gly Ile Pro Gln Gln
4249 TTC GCA TTA AAT TTT GCG AAC AAA AAC CAA TTG CCG GTG TTT TTC ACT TTA TCT AAG GTG ATT TTG GAC TCC GGT ATA CCT CAA CAA
Val Gly Val Leu Pro Val Ile Gly Asp Asp Pro Met Asp Leu Leu Leu Ala Glu Lys Phe Tyr Trp Ile Ala Glu Lys Ser Ser Thr
4336 GTT GGA GTT TTG CCC GTT ATA GCA GAT GAC CCA ATG GAT CTG TTA CTC GCT GAG AAA TTT TAT TCG ATT GCT GAG AAA TCA AGC ACA
551 Gln Glu Ala Leu Ala Ile Leu Tyr Lys Tyr Phe Glu Ser Ser Asn Ser Pro Asp Glu Val Asp Leu Leu Lys Val Glu Val Pro
580 CAA GAG GCA TTA GCA ATA TTG TAT AAA TAT TTT GAA TCA AAC AGT CCA GAT GAA GTT GAT GAC TTA TTA GAT AAA GTG GAA GTA CCC
4423 Glu Asp Tyr Lys Val Asp Tyr Asn His Val Leu Asn Lys Phe Ser Ile Ser Thr Ala Ser Val Ile Phe Asn Gly Val Ile Tyr Asp
609 CAA GAT TAT AAA GTG GAT TAT AAT CAT CAT GTG TTA AAC AAG TTT TCT ATA TCA ACT GCT TCG GTC ATT TTC AAT GGG GTT ATT TAC GAT
638 Leu Arg Ala Leu Asn Trp Gln Ile Ala Met Ser Lys Gln Ile Ser Gln Asp Ile Ser Leu Ile Lys Thr Phe Leu Arg Gln Gly Pro
667 TTA AGA GCA CCA AAC TCG CAG ATT GCA ATG AGT AAA CAA ATA TCC CAG GAC ATT TCA CTT ATT AAA ACT TTC TTG AGA CAG GCA CCA
Ile Glu Gly Arg Leu Lys Asp Val Leu Tyr Ser Asn Ala Lys Ser Glu Arg Asn Leu Arg Ile Ile Pro Leu Glu Pro Ser Asp Ile
696 ATA GAG GGT AGA TTG AAA GAT GTT CTT TAC TCT AAT GCA AAA TCA GAA CGC AAT TTA CGT ATA ATT CCA TTA GAA CCT AGT GAC ATT
Ile Tyr Lys Lys Ile Asp Lys Glu Leu Ile Asn Asn Ser Ile Ala Phe Lys Lys Leu Asp Lys Ala Gln Gly Val Ser Gly Thr Phe
4771 ATT TAC AAG AAA ATC GAC AAG GAA TTA ATA AAC AAT TCA ATT GCA TTC AAG AAG CTA GAT AAA GCG CAG GGT GTG TCT GCA ACA TTT
725 Trp Leu Val Ser Asp Phe Thr Lys Ser Ala Ile Ile Thr Gln Leu Ile Asp Leu Leu Leu Lys Lys Ala Ile Gln Ile

FIG. 1A (cont.)

WO 00/68420

PCT/CA00/00533

4858 TCG CTA GTG TCG GAT TTT ACC AAG TCA GCA ATA ATT ACT CAA TTG ATA GAT TTG TTA TTG CTT CTC AAA AAG AAA GCA ATT CAG ATA
 Arg Ile Ile Asn Thr Gly Asp Thr Asp Val Phe Gly Lys Leu Lys Thr Phe Lys Leu Thr Ala Leu Thr Asn Gly Gln Ile Asp 754
 4945 ACA ATT ATT AAT ACT GGG GAT ACA GAT GTT TTT GGA AAA TTG AAA ACA AAG TTT AAA TTA ACC GCC TTA ACA AAT GCA CAA ATT GAT
 Glu Ile Ile Glu Ile Leu Lys Lys Ser Asn Ala Ser Ser Ala Asn Asp Glu Leu Lys Lys Met Leu Glu Thr Lys Gln Leu Pro 783
 5032 GAA ATT ATT GAC ATT TTG AAA AAA TCC AAC GCT TCA AGT GCA AAT AAT GAT GAA TTG AAA AAA ATG CTT GAG ACT AAG CAA TTA CCT
 Ala His His Ser Phe Leu Leu Phe Asn Ser Arg Tyr Phe Arg Leu Asp Gly Asn Phe Gly Tyr Glu Glu Leu Asp Gln Ile Ile Glu 812
 5119 GCT CAT CAC TCT TTT TTG CTA TTC AAC TCT AGA TAT TTT AGA TTG GAT GGA AAT TTT GGA TAC GAG GAA TTG GAT CAA ATT ATA GAG
 Phe Glu Val Ser Gln Arg Leu Asn Leu Ile Pro Asp Ile Met Glu Ala Tyr Pro Asp Glu Phe Arg Ser Lys Lys Val Ser Asp Phe 841
 5206 TTT GAA GTA TCT CAA AGA TTG AAC TTA ATC CCG GAC ATC ATG GAG GCA TAT CCG GAT GAG TTT AGG TCG AAG AAG GTA AGT GAT TTT
 Asn Leu Val Leu Ser Gly Leu Asp Asn Met Asp Trp Phe Asp Leu Val Thr Ser Ile Val Thr Lys Ser Phe His Val Asp Glu Lys 870
 5293 AAT CTG GTT TTG TCT GCA TTA GAC AAT ATG GAC TCG TTT GAT TTG GTG ACT TCC ATA GTG ACA AAA TCA TTC CAT GTC GAC GAA AAA
 Arg Phe Ile Val Asp Val Asn Arg Phe Asp Phe Ser Ser Leu Asp Phe Ser Ile Asp Val Thr Thr Tyr Glu Glu Asn Ser 899
 5380 AAT TTT ATT GTT CAT GTT AAC AGG TTT GAT TTT AGC TCA TTG GAT TTT TCA AAC TCG ATT GAT GTA ACG ACT TAT GAA CAA AAT AGT
 Phe Val Asp Val Leu Ile Ile Leu Asn Pro Met Asp Glu Tyr Ser Gln Lys Leu Ile Ser Leu Val Asn Ser Ile Thr Asp Phe Leu 928
 5467 CCA GTT GAT GTA ATA ATA ATT TTG AAC CCT ATG GAT GAA TAT TCT CAA AAA TTG ATA AGC CTT GAT AAT AGC ATT ACA GAT TTT CTG
 Phe Leu Asn Ile Arg Ile Leu Leu Gln Pro Arg Val Asp Leu Lys Glu Ile Lys Ile His Lys Phe Tyr Arg Gly Val Tyr Pro 957
 5554 TTC TTG AAC ATT AGA ATC TTA CTA CAA CCA AGA CTG GAT CTG AAA GAG ATC AAA ATT CAC AAG TTT TAT CCG GGT GTG TAT CCT
 Gln Pro Thr Pro Lys Phe Asp Ser Asn Gly Lys Trp Ile Gln His Tyr Ser Ala Gln Phe Glu Ser Ile Pro Ser Asn Val Thr Tyr 986
 5641 CAA CCG ACT CCC AAA TTT CAT TCC AAT GGC AAG TGG ATC CAA CAT TAT TCA GCT CAA TTT GAA AGT ATT CCA TCC AAT GTG ACC TAT

FIG. 1A (cont.)

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Ser Thr Glu Leu Asp Val Pro His Lys Trp Ile Val Val Pro Gln Leu Ser Ser Met Asp Leu Asn Thr Ile Asn Phe Ser Glu Ser 1015
 5728 TCT ACT GAA TTA GAT GTT CCA CAT AAG TCG ATA GTT CCT CAA CTG AGT TCG ATG GAT TTA AAC ACA ATC AAT TTC AGC GAA AGC
 His Ser Val Asp Ala Lys Tyr Ser Leu Lys Asn Ile Leu Ile Glu Gly Tyr Ala Arg Asp Ile His Thr Gly Lys Ala Pro Asp Gly 1044
 5815 CAC TCT GTT GAT GCA AAA TAC TCT CTA AAA AAT ATA TTA ATT GAA GCA TAT GCT AGA GAT ATT CAT ACT GGG AAG GCC CCT GAT GCT
 Leu Ile Phe Arg Ala Phe Asn Lys Asn Tyr Ser Thr Asp Thr Leu Val Met Thr Ser Leu Asp Tyr Phe Gln Ile Lys Ala Tyr Pro 1073
 5902 TTA ATC TTT AGA GGC TTT AAT AAA AAT TAC TCA ACT GAT ACT TTG GTG ATG ACT TCC TTG GAC TAT TTT CAA ATC AAA GCG TAT CCT
 Ser Ile Phe Asn Phe Ser Thr Ser Asn Asp Thr Leu Leu Ser Ala Ser Glu Asn Lys Tyr Gln Ala Asn Thr Glu Leu Glu 1102
 5989 AAT ATT TTC AAC TTT ACT ACG ACC PCA AAT GAC ACA TTA TTG TCT GCA TCG GAA AAC AAA TAT CAG CTT AAT ACC GAG GAA TTG GAG
 Ser Ile Glu Val Pro Val Phe Lys Ile Asp Gly Ser Thr Ile Tyr Pro Arg Val Met Lys Ser Gly Asn Asn Lys Pro Met Leu Thr 1131
 6076 AIC AIT GAG GCG CCA GTT TTT AAA AIT GAT GCA TCG ACC ATA TAT CCA AGG GTA ATG AAA TCT GCC AAC AAT AAG CCA ATG CTG ACG
 Arg Lys His Ala Asp Ile Asn Ile Phe Thr Ile Ala Ser Gly Gln Leu Tyr Glu Lys Leu Thr Ser Ile Met Ile Ala Ser Val Arg 1160
 6163 AGA AAA CAT GCA GAT ATA AAT ATT TTT ACA ATT GCT AGT GCG CAA CTT TAT GAA AAG TTA ACT AGC ATT ATG ATT GCG TCA GTA ACA
 Lys His Asn Pro Ser Leu Thr Ile Lys Phe Thr Ile Leu Glu Asp Phe Val Thr Pro Gln Phe Lys His Leu Val Glu Leu Ile Ser 1189
 6250 AAA CAT AAC CCT AGC CTG ACA ATA AAA TTC TCG ATT TTG GAA GAT TTT GTG ACC CCA CAA TTC AAA CAC TTG GTA GAG CTT ATC TCA
 Ile Lys Tyr Asn Val Glu Tyr Glu Phe Ile Ser Tyr Lys Trp Pro Asn Phe Leu Arg Lys Lys Gln Lys Thr Lys Glu Arg Met Ile Trp 1218
 6337 ATA AAG TAT AAT GTC GAA TAT GAG TTT ATT AGT TAC AAA TCG CCC AAT TTC TTG AGA AAA CAG AAA ACC AAA GAA AGA ATG ATT TCG
 Gly Tyr Lys Ile Leu Phe Leu Asp Val Leu Phe Pro Gln Asp Leu Asn Lys Ile Ile Phe Ile Asp Ala Asp Gln Ile Cys Arg Ala 1247
 6424 GCG TAT AAG ATT TTG TTT TTG GAC GTT TTG TTC CCA CAA GAT CTC AAC AAG AIT ATA TTC ATT GAC GCC GAT CAA ATA TGT AGG GCA
 Asp Leu Thr Glu Leu Val Asn Met Asp Leu Glu Gly Ala Pro Tyr Gly Phe Thr Pro Met Cys Asp Ser Arg Glu Glu Met Glu Gly 1276

~~TABLE~~ - IA (cont.)

FIG - 1A (cont.)

376 PDGALFNGCLFFDADTNDLVSLIETLRSEBRVIESHSNNYRGSIASSTFLLDTASSKKEFAIDIR-----D TAVQMVN
 DmUGGT
 335 EGFNIMINGASLDLEEDAFSICSLINBETONFDRFEALGKSSKVLNIVIEHEPABEDSDFKVBFHCQDDIED-----W KATHMVN
 SpUGGT
 351 QDSICPTINGSPILPLEDITVNGTRIKESITWKTIVKGFDTVQAKULIKFIALLSAVKQIQFRNGRTANGNWNFKVTENEFKKGSSEKCGGLFFFN
 CaXRE5
 333 YMLGLYNGQNHKITSITPYMNTTAUKTEIQSMLKTIINLQELEFENQIDS KFLHKKFSQFSLGLLQHQQPKKNDLHTIPG-----FSESIVTFN
 scKRE5

SUBSTITUTE SHEET (RULE 26)

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452 DIENDVQYRRHPSVMDLLE-----PTFPCLRNHRKRVFHLVAVLALGTAASVTKLSESVHQAPEFRIGLIFDARDAMEDHADYVATCATYHVS
419 EIESNEKYDWHPSIQILAK-----PIIPGOLHNLGNQLHVIPIPPSPSSDPLUSDAIOFSRRPSPVQIGVCAAMDDDE-----FAQIVCKSEFFYIS
451 XIELDNEXEETTDREAYLGVSXKXKXNFIPLIKENIHDLIFNLTFGKXHQANFFTLCKVILDSGIPQOVGULPVIQDDP-----MDLLUAEXFFYHIN
425 DIESDPQYDELVNSVQAFD-----KXVFGELPEIKONKSEILFVIDEHLLEDSPKEALGGLVRAVHVSQGYPORVGLLPFS-----SDSKSVVUKIY

547 OKKDAARASFLTDIYNAVGETXVVKXNDIVKQATKEFTSLSF AKAEZFLLEDSTIDYCRELA AEFIORLGFQDKEQPOALLNCPMPSPSVVUTADSDFFE
510 KESGDSALFELYNQNSDSSADLISGEEHLPLSEHDDDTLAKKXOLS--SSFFDHVKSXSNMVRRLGIDSS-----AS EUTVNGRIISHOENYDR
547 EKSSTOEALAILYKTFESHSPDEVDLADKVEPEYKVDYHHVWAKXSUSIASVIFGCVYD-----LR--APHWQHA-----
516 ELKNSTONLCEZKSFLETHLADGTSANANXKHIPVP-DVPHILLDELQDEHISJINGELYP-----FRXNN-----Y

647 NIFTEINHTSMLOKAVIKGELIDN-DVAIDEMXQHVMPRLNQRILSQEDUKYLDINGVAYKNLGNVGVNRLSHNRMTATLADNLKVFCKKKSTELI
602 SWYGLFELDIPEVQITVAEICKISED-DHALDRLRDLQSNRNP LWTESAKSISIDIKRULEN-----VGSJNHEDILLIGSSNAKYS-----
619 KSKQUSQDISLIKTELROCPJEG---RUKOVLYSEKSENRLRDLPLEPSDIYKKKIDKELIN-----NSIAFKKLDKMQGVSG-----
585 LIAKQKKTOTEFIRHELSWSSPKXKQISVRDILAHYKSAHNNKXITPHIFADS VYSSVNNHLES-----VCSERIGITYKNEEN-----

746 GRISLOPLINVFADLETDQCRDLATHALDIWQSGESVHVAFTPHTESSASSRRNCHNVMANHOGLPFIQATEQVULKWKKPUENIEIPQLEDILGS
685 FHLVADNEKEGELEILSLADLISENKDANLLO-----EGXNHVVPPLFAKLSSPKSSKHGCELAN-----SSLDPSGCVVNDQDK
695 EPHVNSDTKSAHITQIDILALAKKKAQIRLHIG-----DIDVFGKQKTKFHTTALINGQDEHIELAN-----KSAASSANDE
666 LLHNTLAVDDEGSHVZKRLRNLLHTSFVGVRIHNVG-----DISDHYQURGSLSQKDEIGSINTFIDALKLKRVKSHTYKXSGIWLQ

846 TELHLMGLRVESORVLEQHNKSORLVVGNCRUTYCPSSDESFSADFMILARFSLQVSDKVRQVLKESNQDVN-----EEFNSDTLLKLYASLDPRQ
765 ALKFLAKKSAVVKRELGITGECKSALLNGRMVICSFSVDS-LHIALDKQVQKQETDEYLSKLSH IAGSSRRKXSRATFSLSSTLKLESTPKS TSSPIKE
773 LKXMLETKQPAHHSPFPHSRIFRLDGHFGVEELDQIIIEVVSQRLHLPDI MEAVPDEFSKXVSDPHVLSG-LDNMDWFDIVTSIVTKS FHVDEXR
753 LKXWLPDIEPHELOKGSFIALNGRFLILKXWQCKQKISKAKI IYREARHRTDSVFALDILFPFGFSQEIINPDILIEHMISSILTRIFYQGTHLYNNGIDYT

FIH - 1B (cont.)

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DmUGGT 938 TKTRFKLPTDLDJHSVVKLPPKQEKLPHPDVARVLDPASRAAQKLPITILDLRQVYHQQDMLTIDIP-VPOHSDQPVKNFYR-YVVEPAVQFEANGCRSD
 SpUGGT 864 EKLFPROFIDHKLGVGMATFEDDFSKATIQFVAVLDPLSKDSQNSAILEAVSKHCGVRHHP-KQILSELPLTRFYR-VSISABEDALG-HLE
 CaKRES 872 FIVDVARFDISSLDFSNSTQVYIIEENSPDVLLIIEPDEYSQKLSLVNSHIDFELNIRIILQCPVOLDKEEIKHIFYRGVYPOPTPEIDSNCKMIO
 ScKRES 853 HESSLPANDLSEFFRPNMUTYFEDGKASSTDLILLDPLEERTQXELSLVBOFPAKFNUNIOVILAP-----TLELNIVIPIRRIYUDDADIVKSIYS-----

DmUGGT 1036 GPIAKFSGLPANPLLTQOLQVPEHMLVEAVRAMYDLDVNIKLTIDIGG-----PVHSEFPEMLLECHCFDASGAPPRGLQVLCIQSQPTLVDTAVAN
 SpUGGT 961 ESYVEFDNLPADTLQNDIEARPANTVQQDVDDIDFNKLEHTSEAEALDSHTATHEVKNLLVQCHSQEFRKSPPRGQDKLGNLTNSHVTDQIVLSN
 CaKRES 972 HTSACFESTPSNVTYSTELDVPHKHIIVVQSSWDIHTHFSEHS-----VDKYSLSXN-JLIEGYARDIHTCKAPDGLIFRAFN--KMYSDDLVHYS
 ScKRES 945 ----EDS---RSDPEMDIENOVENSFIUDHNTIRUKKILIELHSFSSK-----TVLSYGNIDGNGCVCTATVQSAGHIDKATTKT

DmUGGT 1111 LGYFQKLANPGMWSRLRECKSADIVATSHIEGNNRMSAGSSEVQVLDLSLRSHVVKLWMSKPKQKQCAELLSDDMEQAAQSCHNNSASSFCGGSANQ
 SpUGGT 1061 LGYFQKLANPGVMTLEPHDGRSSQFVEILSLHKNNSQOP-----QVINDSFEGVTHPPWMPKPKQFESNDIMQEDLSSEKFFDKIKKLSLSPFN-----
 CaKRES 1064 LDYFQKHPYSIHNFTST---TSH---DTLSASENQQAN-----TEDEESTHPVFKNIGSTIYPRVMSGNKPK-----
 ScKRES 1019 FGICQPHDQKFLKGCYIKSCDRIYVQSFSTPHPPDIPS-----DSQDILSYNPKIYAVKISEPTHEEEYEFG-----

DmUGGT 1231 AASDEDETINIFS VASG--HLYERLIRIMVSLDKHT-KSPVKFQFLKX-JLSPOFTDQLPHMAS--PXNFQVEADQYKWRWLKQKTEKQRTINGYKI
 SpUGGT 1150 --FKRMENSINIFS VASG--HLYERPLIINTKSVLEHT-DKXKEMFTEN-FLSPCFNSSIPALAK--KINFEYETITYNPHHLRKQEKQREINGYKI
 CaKRES 1129 -MLTRMHDINIFT IASG--OLYEKLTSLMTASVRKHHFSLWKFKHLEK-FVTPQFKHLMELISI--KXNVEVEFISYKWPNDLKKQKTHPRMTHGYKI
 ScKRES 1089 ---RNNQDITINIFI ILESQPDDEERTMOMILSLSKCPKQKVNFEHIDQPEISDILKXSCETINSSDENRGNVFEDNYEHPQHLPEQRFSSRRRDVSRF

DmUGGT 1325 LFLDVLFPPLNVRITAVDADAIVRTDKELVDNDLGGAPVYTFECDSKXENEGERFNKQGYNRSHMLG---RKHISALIVVDLKRFRKTAAGDLRGO
 SpUGGT 1242 LFLDVLFPPLNVRITAVDA-QIVRADLOELQNDLEGAPYGEPRCCSKXENEGERFNKQGYNKKFLRG-----LKHISALIVVDLDRFRKMGAGDLRRO
 CaKRES 1223 LFLDVLFPPLNVRITAVDADOICRADITELVMDLEGAPYGEPRCCSKXENEGERFNKQGYNKKFLRG-----LKHISALIVVDLQKFRSTKAGDLRAH
 ScKRES 1186 LFLDVLFPPLNVRITAVDADOLYNSPTNPLDPFDIFQFQGLKRAFLGLFRLS-----GDGHNKEGYNEMLENNHLEFVSTEPAFIVLELFRFRLDAGDKYRIH

-----1B (cont.)

11/24

DMUGGT 1422 YQALS QDPNLSNL DQDLPNM IN QVNI KSLPDD HLCCTWCS DSIFKTA VI DLCNHPCKE AKU TAAR IV PEHNDYD NEL KTL MSRI EDHENS HRD
 SPUGGT 1338 YQLLS ADPNLSNL DQDLPNM ION DIPYISLPD HLCCTWCS DESIKTAK I DLCNPLKE KKD PARR OV SEHTSYDNEI ASVLOTAS SQ SDMEFEI
 CAXRES 1321 YQKLS SDPNLSNL DQDLPNM QRLIKI HPSLPD HLCCTWCS DKSLEDAK I DLCNHPLE PEHNDARKRLI PEHMEYECEI EPLVSLVQNH TAMBVVQ
 SCXRES 1279 YQRTIS QDAMSLVNI QDILVNNI QLEVPJR ----- FLKG--S ----- YKRLVINDECV SEHKKK INK FASSPGDECV PGESVSK

DMUGGT 1522 SAVD DSVD DS VEVT TVTPSH EPRKH GEZ
 SPUGGT 1438 KDNN SSPDEL -----
 CAXRES 1421 EHEH DZGCEQEFQK QESND DDFI HDEZ
 SCXRES 1352 YQDS DNAA PPHDEL -----

7 1 8 7 0 5 (cont.)

7-10-11

319	Glu Phe Ile Arg Glu Glu Arg Glu Glu Tyr Leu Gln Lys Gln Met Ile Ala Lys Asn Ile Leu Arg Ile Asp Glu Phe Gln Asn	319
1208	GAA TTT ATT AGA GAA GAA GAA GCT TAT TTA CAA AAA CAA ATG ATT GCT AAA AAT ATT CTG CGT ATT CAT GAA TTT CAA AAT	1208
1295	Leu Ser Lys Asn Asn Thr Thr Ser Ser Gly Ala Ser Arg His Pro Tyr His His Ser Asn Asn Lys Lys Asn Asn Gly Gly Asp	348
1295	TCC AAA AAT AAT ACT AAT GGT GCA TCT CGT CAT CCA TAT CAT CAT CAC ACT AAT AAT AAA AAT AAT GGT GGT GAT	1295
1382	Gly Gly Ser Ser Met Ala Ala Leu Lys Tyr Thr Pro Lys Asn Ile Leu Lys Lys Thr Leu Ser Arg Phe Glu Phe Thr His Glu	377
1382	GGT GGT GGT TCT AGT ATG GCA GCA TTA AAA TAT ACT CCA AAA AAT ATT TTA AAG AAA ACA TTA TCA TTT GAA TTT ACT CAT GAA	1382
1460	Asn Ser Ser Ser Glu Glu Ile Tyr Glu Leu Lys Thr Lys Gln Gln Pro Tyr Lys Tyr Asp Asp Gln Leu Ser Leu Thr Ser	406
1460	AAT TCT TTA TTA TCA GAA GAA ATT TAT GAA TTA ANG ACT AAA CAA CCA CCT TAC AAA TAT GAT GAT CAA TTA TCA TTA ACT TCA	1460
1556	Ser Thr Ser Ser Thr Ser Gly Ser Gly Ser Gly Gln Val Lys Phe Gly Gly Ala Arg Ile Ser Asp Gly Ile Asn Gly Gly Ser Leu	435
1556	TCT ACA TCT TCT ACT TCT GGA TCT GCA TCT GCG CAG GTG AAA TTT GGT GCA GCA AGA ATT TCT GAT GCG ATT AAT GGA GGT TCA TTA	1556
1613	Pro Asp Arg Phe Ser Leu Phe His Ser Glu Ser Glu Thr Ile His Ala Pro Asp Ile Pro Ser Leu Val Ser Pro Gly Gln Ser	464
1613	CCT GAT AGA TTT TCA CTT TTC CMT TCT GAA TCA GAA GAA ACT ATT CAT GCC CCC GAT ATT CCA TTA GTA TCA CCA GGT CAA TCT	1613
1730	Val Arg Asp Leu Phe Arg Asn Gly Glu Glu Thr Trp Trp Leu Asp Cys Thr Cys Pro Thr Asp Ser Glu Met Lys Met Leu Ala Lys	493
1730	GTT CGA GAT TTA TTT AGA AAT GGT GAA GAA ACT TCG TCG TTA GAT TGT ACT TGT CCT ACT GAT TCG GAA ATG AAA ATG TCG GCG AAA	1730
1817	Ala Phe Gly Ile His Pro Leu Thr Ala Glu Asp Ile Arg Met Gln Glu Thr Arg Glu Lys Val Glu Leu Phe Lys Ser Tyr Tyr Phe	522
1817	TCT GAT ATT CAT CTT TTA ACT GCT GAA GAT ATT CGA ATG CAA GAA ACT CGT GAA AAA GTT GAA TTA TTT AAA AGT TAT TAT TTT	1817
1901	Val Cys Phe His Thr Phe Glu Ala Asp Lys Glu Ser Glu Asp Tyr Leu Glu Pro Ile Asn Val Tyr Ile Val Phe His Asp Gly	551
1901	GTT TGT TTT CAT ACT TTT GAA GCT GAT AAA GAA TCT GAA GAT TAT TTA GAA CCG ATA AAT GTT TAT ATT GTT TTT CAT GAT GGT	1901
1991	Ile Leu Thr Phe His Phe Ser Pro Ile Ser His Pro Ala Asn Val Arg Arg Val Arg Gln Leu Arg Asp Tyr Val Asp Val Ser	580
1991	ATA TTA ACG TTC CAT TTT TCA CCA ATT TCT CAT CCA GCA AAT GTT AGA AGA GAT CCA TCG AGA GAT TAT GTC GAT GTT AGT	1991
2078	Ala Asp Trp Leu Cys Tyr Ala Leu Ile Asp Glu Ile Thr Asp Gly Phe Ala Pro Val Ile His Gly Ile Glu Tyr Gln Ala Asp Ala	609
2078	GCT GAT TCG TTA TGT TAT GCC TTA ATC GAT GAA ATT ACC GAT GGT TTT GCC CCC GTG ATT CAT GGA ATT GAA TAT GAA GCT GAT GCG	2078
2165	Ile Glu Asp Ala Val Phe Thr Ala Arg Asp Thr Asp Phe Ser Ser Met Leu Gln Arg Ile Gly Glu Ser Arg Arg Lys Val Met Thr	638
2165	ATT GAA CAT TAC GTT TTC ACT GCT ACA GAT AAT CAT TTT AGT AGT ATG TTA CAA AGA ATT GGT GAA TCA ACA AAA GTC ATG ACT	2165
	Leu Met Arg Leu Leu Ser Gly Lys Ala Asp Val Ile Lys Met Phe Ala Lys Arg Cys Gln Glu Ala Asn Ser Ser Ser Gly Tyr	667

FILE - ZA (cont.)

FREE - ZA (cont.)

15/24

ScALR 1 1 MSSSSSSSSSPALSRNSLSTANWVSMKTDHDTGLIDHROHPC
ScALR 2 1 MSSLSSTSPDSSDLPRSKSVDTAISMKWCXPKLENIRQISDA
CaALR 1 1 -MSDSESITQHSITNOPIPRSDVDDHHRHQTNDCAISDSED

ScALR 1 100 GODETVANHOLRNSAILTSNARPSRLAMSHHQRLQVESH
ScALR 2 99 AEAELVXRYQLRSFALISSNARPSRLAKSDHOKQURVESTAPLEKN
CaALR 1 92 -KDRITHPMSUGGDDTINSCHKHRYNNSDRLKDPYUKND

ScALR 1 196 ESKSDTHSLANPKKRTYSTISNHSINPAVLLTKSSOKSDA
ScALR 2 195 ESEHGHFNCAKPKRTYSTISTHSSVNPILLERISOKSDHGP
CaALR 1 191 DLVSPHAKKINDSEDIINTSITANMKXUGIGATIDVGIGI

ScALR 1 295 EEVAQFAN-----AEKSOPLASTQVPHQK-----
ScALR 2 294 EEVAQISN-----AERVLSLANHQHRSRT-----
CaALR 1 290 DEFIREEREATLOKQOMIANKVLRIDEFQNLKNNHTISGASHP

ScALR 1 368 EDEHEKIKPSLRHGISTCKNNKVEGEENENIPSDPAYCSIGCTD
ScALR 2 367 ESVREDDKPDLRHDVTFGRNNKEGEKENDSSISRATITQTEIO
CaALR 1 390 TKQQPPKMDQDLSLTSSSISTSGSGSQVKFGG-ARISDGIN

ScALR 1 468 RCIAKAFGINPLTAEDIRHQETREKVELFKSYFVCFHCFENDKE
ScALR 2 467 RCIAKFGINPLTAEDIRHQETREKVELFKSYFVCFHCFENDKE
CaALR 1 489 KQAKAFGINPLTAEDIRHQETREKVELFKSYFVCFHCFENDKE

22

10/018105

16/24

ScALR 1 568 IDDI TDSFAPVIO SIEYEADATED SVFMARDNDF AANLORIGE SRRKNTLNR LLSGKADV KFAKRCODEANGIGPALTSO IN DANLQARDQD-----
 ScALR 2 567 IDDI TDSFAPVIO SIEYEADATED SVFMARDNDF AANLORIGE SRRKNTLNR LLSGKADV KFAKRCODEANGIGPALTSO IN DANLQARDQD-----
 CaALR 1 589 IDDI TDSFAPVIO SIEYEADATED SVFMARDNDF AANLORIGE SRRKNTLNR LLSGKADV KFAKRCODEANGIGPALTSO IN DANLQARDQD-----

ScALR 1 662 IDDI TDSFAPVIO SIEYEADATED SVFMARDNDF AANLORIGE SRRKNTLNR LLSGKADV KFAKRCODEANGIGPALTSO IN DANLQARDQD-----
 ScALR 2 661 IDDI TDSFAPVIO SIEYEADATED SVFMARDNDF AANLORIGE SRRKNTLNR LLSGKADV KFAKRCODEANGIGPALTSO IN DANLQARDQD-----
 CaALR 1 689 IDDI TDSFAPVIO SIEYEADATED SVFMARDNDF AANLORIGE SRRKNTLNR LLSGKADV KFAKRCODEANGIGPALTSO IN DANLQARDQD-----

ScALR 1 714 IDDI TDSFAPVIO SIEYEADATED SVFMARDNDF AANLORIGE SRRKNTLNR LLSGKADV KFAKRCODEANGIGPALTSO IN DANLQARDQD-----
 ScALR 2 713 IDDI TDSFAPVIO SIEYEADATED SVFMARDNDF AANLORIGE SRRKNTLNR LLSGKADV KFAKRCODEANGIGPALTSO IN DANLQARDQD-----
 CaALR 1 789 IDDI TDSFAPVIO SIEYEADATED SVFMARDNDF AANLORIGE SRRKNTLNR LLSGKADV KFAKRCODEANGIGPALTSO IN DANLQARDQD-----

ScALR 1 813 IDDI TDSFAPVIO SIEYEADATED SVFMARDNDF AANLORIGE SRRKNTLNR LLSGKADV KFAKRCODEANGIGPALTSO IN DANLQARDQD-----
 ScALR 2 812 IDDI TDSFAPVIO SIEYEADATED SVFMARDNDF AANLORIGE SRRKNTLNR LLSGKADV KFAKRCODEANGIGPALTSO IN DANLQARDQD-----
 CaALR 1 885 IDDI TDSFAPVIO SIEYEADATED SVFMARDNDF AANLORIGE SRRKNTLNR LLSGKADV KFAKRCODEANGIGPALTSO IN DANLQARDQD-----

----- 2B (cont.)

1
52 TGAATTGTATGGATTGTTAACAATAAGATCATATTGCTGGTGCAGCGGAATGGCACAAGATAAAATTAAGAAGTCACCTCAGCTCAAAAACAAGTTGTTGAGAAATATTTCC
167 AATTGATACCCCATGGCAACCACAGAGGAATTTCTCAGCTGAATGGTTGAAATTTTATGAAATGGTGCCAGATTACTCATTTGGCATATGGGCAGGTACCATTTTAGGATT
282 TGAGCAAGAATATGAGAACATCATTTGGAGAAATACCATGCTAATGATGCTCTGTCAAATAAACAATGAAAGATATCGAACATGAGTTGTTACATCATCAACAAGAG
397 ATTGAAGAGACTCACGATAGATCGAGTCGATTGMAAAATTTGCTGGTGATTACTGGTCAGAGATCAATATCGACAAATCTTAAACCAAATATAGAAAAACAACAGAAATAGTAGAG
512 AGGTTAGTAAAGAGAAACCTTNAAAACACACCAGGAAGCCAACNCTAGCTTGGCTATATAGAAGTAGAAATAGAAATCANGATCAATAAAAAGACGCCACCAACAGCGCTACTACT
627 ACTACTACATTTGAAACAAATTTGCTGGGAAGTTGAATGATTGCACATGTGAGCCACATAGCTTAGGTATAGTTGCTTGAACCTAAACACCGAAGTTCTTGTATTAAAGATAG
742 AATTCCTCTCTCTCAAAAAGCTCAAAATTGACACACACAGTAGAAGTATTTTTGACGGGTATATTGGCAAGTCAAAATGAATGTGTGTCATTTCAATCTCTACAAAAGATACA
857 AAAATCAATPAAACGAATTATATAATAGTTGTCATCATCGTCAAAATAAGCAGAAAAATTACATTTATCCTATGGAATTGTAATGTGATTATGATTAATGCTTGAATTTGAGGTCGTA
972 GTAGTAGTAGCTGTGTTTCATTTATGCAACATTAACCAACATACAGAACATAGAGGGGGGGAGGAATTGATTGCTCTACTAGTTTCTTATTACAAGAANTTTCTTTTG
1087 TTTTAGAGTAAATTAATGATATGATATGATGTAATGTTTCAAAATGATTTTCAATTAATTTTCGCTACAAAAGAAAGAAATGAAAGAAATTTTCATTATGGA
1202 ATTTTGGGGATTAAGAATGCTGGTTAAATFACCTTTTGCTATTCAATTCAGCTTGAGTTTACTAGTTTGCACCTGGTTGCCACTAGTTTGGCCACCAAGAAGTTG
1317 GACTAAAGTTTATATCTCTTATATATAATTACCTTAATAGTCAACTTCCTTCTTCAATTCCTTGTAGTCTTTGTTACATTTTGTGTTCTGTTCTGTTACTAACAAC
1432 AACACAATATTTTTTTTAAATCCCTCCTCACTCAATCAACACACACACCCCTATTTCTTTCTCTTCTACTCTTGGTGTAACCTTTTGGCTGGCCTCTTCTTTTG
1547 CTATTTTCAAATTCATTTTGTAGCTCATTTTAAATTTATTTCAATTTGTTTCCATTTATTTCCATCTTTGCTTTTCCATTTATTTATTTTCTTTTGTAGTTAGCT
1662 CTAATTCNACTTCTTACTCTCAACTCGAAATCTAACAACTAAAAAAGACAGAGTGAAAAAGGTGTGAGAAATTTGCTRAAAAAAATAGACAGACAGAAAAAGAAAGTTA
1777 ACGMACCAANGACAGGAGAMAAAAANATCCACACAGGACAAACATCAACAAACATTACATCAGCAACAGACAGACCAATATACATTAAACCAATCACACTGAAC
1892 TTACTCATAACTACTGCTCATATCTTCTCTTTTTTTTTTGTGTCATATTGAAGAAATAGAAACCAATAGAACCACTCATTTATATCTTAATATCAACAATCCAAAC
Met Glu His Pro Ala Ala Leu Arg Thr Phe Ser Thr Gln Ser Thr Ser Ser Leu Asn Ser Val Ser Thr Val Ser Ser Ser Arg
2207 ATG GAA CAT CCA CCA GCA GCT CTC AGA ACA TTT TCA ACC CAA TCA ACT TCA TCT TTG AAT TCA GTA AGT ACT GGT TCG TCT TCA AGA
Ile Val Ser Leu Gly Pro Val Asn Ile Asn Asn Phe Asn Lys Pro Ser Thr Pro Lys Asp His Leu Phe Tyr Arg Cys Glu Ser Leu
22094 ATT GTT TCT CTG GGC CCA GTC AAT ATA AAC AAT TTC AAT AAA CCA AGT ACT CCC AAA GAC CAT TTA TTC TAT CGA TGT GAA TCA CTA
Lys Arg Lys Leu Lys Ile Pro Gly Met Glu Pro Phe Leu Asn Gln Ala Phe Asn Gln Ala Glu Gln Leu Ser Glu Gln Gln Ala
22181 AAA CGA AAA CTA AAA ATC CCT GGC ATG GAA CCA TTT TTG AAC CAA GCT TTC AAT CAG GCT GAA CAA CTC AGT GAA CAA CAA GCA
Leu Ala Leu Ala Gln Glu Arg Ser Asn Gly His Ser Asn Gly Lys Arg His Gln Ser Leu Asp Gly Ala Met Asn Arg Leu
22268 TTG GCT TTG GCA CAG GAA AGC AAT GGA NAT GGA CAT AGT AAT GGC AAA CGT CAT CAA TCA TTA GAC GGT GCC ATG AAT AGA CTT
Ser Val Gly Ser Asp Ser Ser Ile Gln Gly Ser Leu Thr Arg Met Ala Thr Asn Ala Ser Thr Ser Ser Leu Ile Ser Gly Met
2355 TCA GTT GGT TCT GAT AGT AGT TCG ATT CAA GGT TCA TTG ACA CGA ATG GCT ACC AAT GCG TCA ACG TCA TCT TTA ATC AGT GGT ATG

FILE 7A

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File - 3A (cont.)

FEB - 5A (cont.)

484	CaCDC24	GFMIDAGGELLFHHGQVGVKDDH	-----EKEVVAFLFEKIVFFHEDDKKISDKQVKKSNFSRRKR-----STSSNLS
476	ScCDC24	GRTDSKFGELLIFDKVHUSTHSSSEPEREFVYLEEKIITLHFHWKFA88LILINKVSSASAS	-----ISASNTIDKNGSPHH-----
386	SpCDC24	GYSIQIFGCLLVHDDVWVVCDDI	-----EREYHVLFPEKILLCCHEMSLRRQARSLSHKNTVRLDLSLQKGRILTSNITVVPHHNGSIAIQIFWRGD

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CaCDC 24 553 -----SSITMLPSIHNRKQALP-----DEKGRVISETHISAPNTEGS-----
 ScCDC 24 557 -----SYKXGNSSSSNWHLSSSSAAATKSSSTKSDTHSSSSSSLPKLSAHEPKDARGHIMKMLQIIPQNR-----
 SpCDC 24 482 PCHESFILKLARNEESHKELMSVLNRLWKNEHGSXPDKRSAASTPAPVTHRSSQISKGYHSSDIYDLETHSDENVNSPTISISFSSKSSPFFKTSK

CaCDC 24 597 LIISMSGRKESGFTLHYRSEELRNQHEKCIARDPKYHETKQLEKMLTSDLSFHDSDSIIYDTGISTSPVNOSSQOQYIDHRGSHSSRHSSSSSLSH
 ScCDC 24 633 LNIWESIKEQCNFLKFKNEETDMSSCLOQLINDUKNEQFMWHESS-----TSTTSSWAKSSSXSPQTHMTPTTHMSRQTHDSWSTSSSH
 SpCDC 24 582 DTKSATTTDERPSDFURLNSEESVGTSSLRTSQITSTLYSHDSSSTASIPSQISRISQVMSL LNDINYNROSHIRVYSGTDGSSVSIFDDTSSSTKQK

CaCDC 24 697 WKHHRVKSGDLRSISSTILDSTSNLNGSPHTNPSLESSDARKPPFDVAIKLTKSTELSEPLIYVAQIEYHLLQKISQIITSN--LVADDVN
 ScCDC 24 725 WK-----RVSDVLPKRRTHSSSESEIKSISEYFKSIPESSLPRTSYHNSHNTSSSEIFTDVEKVNHTDDUHAHESKISNT--HNHTSP
 SpCDC 24 682 QPDQPTINDCDVHRPROTSISAGHXSGDGLPSFKHTSLSSSTGSSSTVHTVVKTRLRRLHEVSLVLVAKDITFEDDLAKVHKKIKLGGIPKQWPPF

CaCDC 24 795 ISRLRYKDDGDFVNLNSDDMGVLDMLTSDFIQTSSEKRLVITVUS---
 ScCDC 24 813 LKIKVQDEGDFVVLGSDENHVAKEHFAENKFFHRLI-----
 SpCDC 24 782 RVRKXVDEGDFLQTSDEQVLHAFETCTELHDPMHNGCHDVLHVVVF

--- 3B (cont.)

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CaKRE5 1 2 3 4 hisG 1 2 3 4 CaURA3 1 2 3 4

9.0 kb-
5.0 kb-
5.0 kb-

Fig. 4B

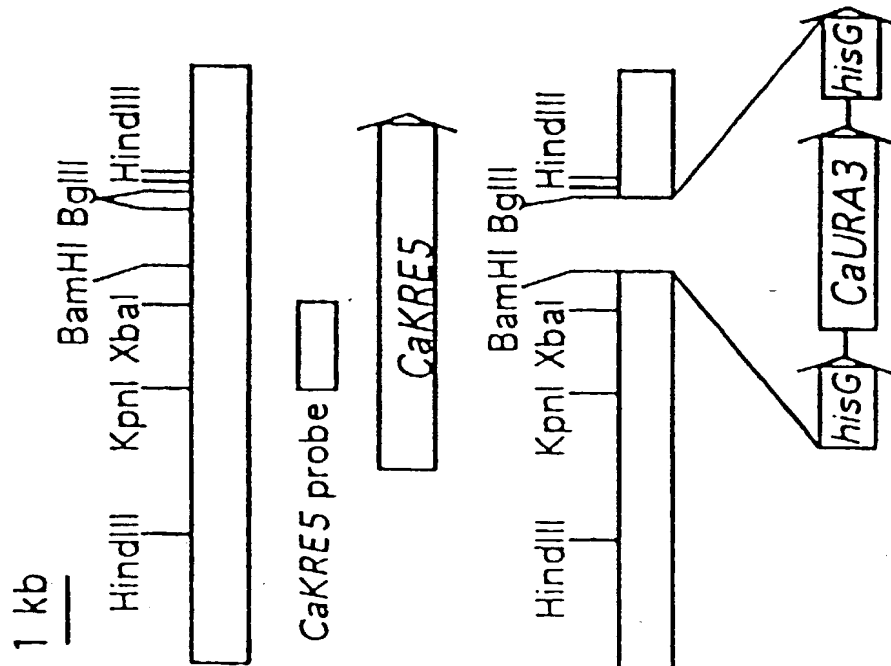


Fig. 4A

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PCT/CA00/00533

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CaALR1 hisG CaURA3
1 2 3 4 1 2 3 4 1 2 3 4

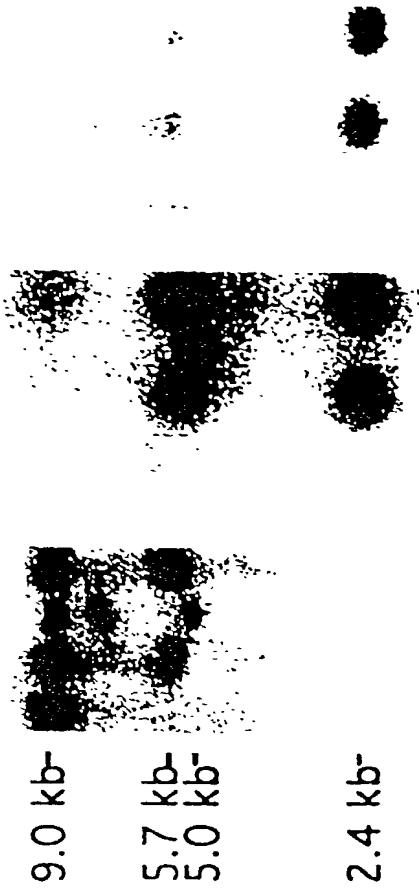
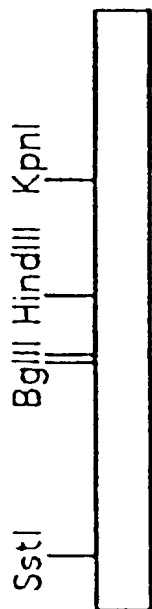


FIG. 4D



CaALR1 probe

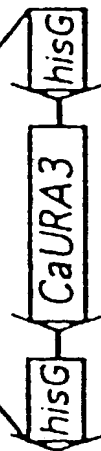
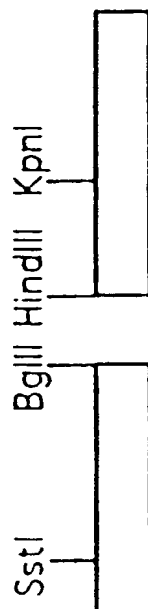


FIG. 4C

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PCT/CA00/00533

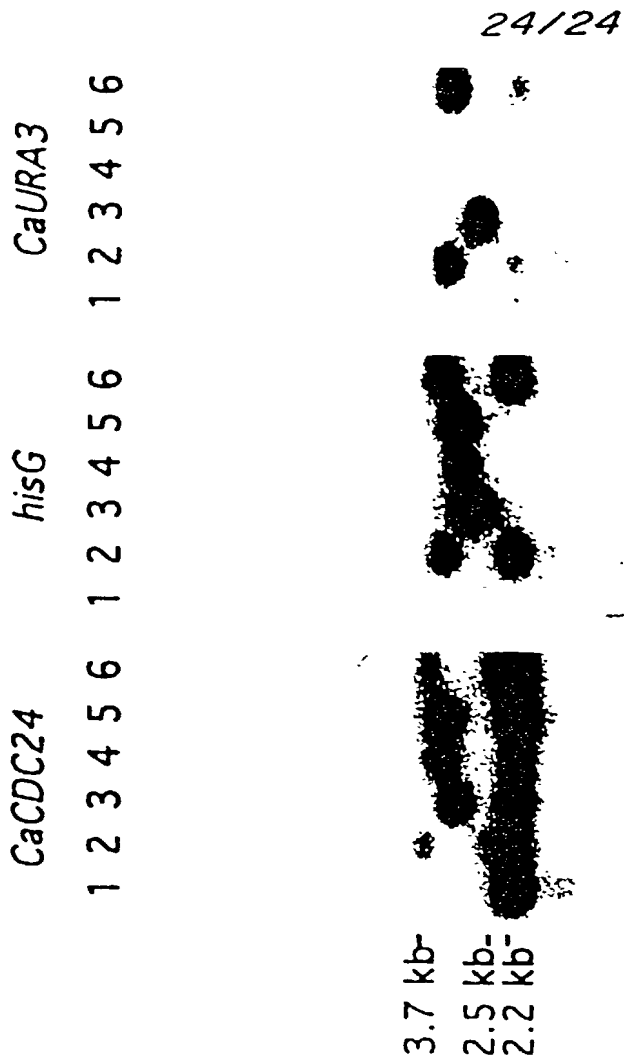


Fig. 4F

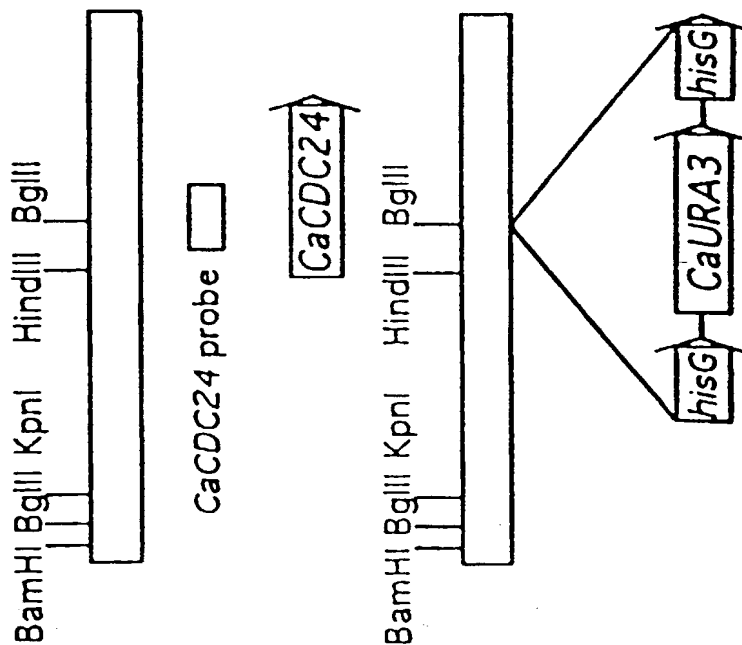


Fig. 4E